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1120 ~~77~~ 8



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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/043,649

DATE: 12/02/2002
TIME: 15:08:54

Input Set : A:\EP.txt
Output Set: N:\CRF4\12022002\J043649.raw

3 <110> APPLICANT: Holland, Sacha J.
4 Mendenhall, Marcy K.
5 Pardo, Jorge
6 Spencer, Collin
7 Fu, C. Alan
8 Luo, Ying
9 Payan, Donald G.
10 Mancebo, Helena S.Y.
11 Wu, Jun
12 Zhou, Xiulan
13 Shen, Mary
14 Liao, X. Charlene
15 Sheng, Ning
17 <120> TITLE OF INVENTION: Cloning of a Novel Inhibitor of Antigen-receptor Signalling

by a

18 Retroviral-based Functional Screen
20 <130> FILE REFERENCE: A-70219-1/RMS/DHR
22 <140> CURRENT APPLICATION NUMBER: US 10/043,649
23 <141> CURRENT FILING DATE: 2002-01-10
25 <150> PRIOR APPLICATION NUMBER: US 60/260,953
26 <151> PRIOR FILING DATE: 2001-01-10
28 <160> NUMBER OF SEQ ID NOS: 3
30 <170> SOFTWARE: PatentIn version 3.1
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 786
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)..(786)
40 <223> OTHER INFORMATION:

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44 Met Gly Ser Leu Pro Ser Arg Arg Lys Ser Leu Pro Ser Pro Ser Leu
45 1 5 10 15
47 agt tcc tct gtc caa ggc cag gga cct gtg acc atg gaa gca gag aga 96
48 Ser Ser Ser Val Gln Gly Gln Gly Pro Val Thr Met Glu Ala Glu Arg
49 20 25 30
51 agc aag gcc aca gcc gtg gcc ctg ggc agt ttc ccg gca ggt ggc ccg 144
52 Ser Lys Ala Thr Ala Val Ala Leu Gly Ser Phe Pro Ala Gly Gly Pro
53 35 40 45
55 gcc gag ctg tcg ctg aga ctc ggg gag cca ttg acc atc gtc tct gag 192
56 Ala Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile Val Ser Glu
57 50 55 60

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59 gat gga gac tgg tgg acg gtg ctg tct gaa gtc tca ggc aga gag tat	240
60 Asp Gly Asp Trp Trp Thr Val Leu Ser Glu Val Ser Gly Arg Glu Tyr	
61 65 70 75 80	
63 aac atc ccc agc gtc cac gtg gcc aaa gtc tcc cat ggg tgg ctg tat	288
64 Asn Ile Pro Ser Val His Val Ala Lys Val Ser His Gly Trp Leu Tyr	
65 85 90 95	
67 gag ggc ctg agc agg gag aaa gca gag gaa ctg ctg ttg tta cct ggg	336
68 Glu Gly Leu Ser Arg Glu Lys Ala Glu Glu Leu Leu Leu Pro Gly	
69 100 105 110	
71 aac cct gga ggg gcc ttc ctc atc cg ^g gag agc cag acc agg aga ggc	384
72 Asn Pro Gly Gly Ala Phe Leu Ile Arg Glu Ser Gln Thr Arg Arg Gly	
73 115 120 125	
75 tct tac tct ctg tca gtc cgc ctc agc cgc cct gca tcc tgg gac cgg	432
76 Ser Tyr Ser Leu Ser Val Arg Leu Ser Arg Pro Ala Ser Trp Asp Arg	
77 130 135 140	
79 atc aga cac tac agg atc cac tgc ctt gac aat ggc tgg ctg tac atc	480
80 Ile Arg His Tyr Arg Ile His Cys Leu Asp Asn Gly Trp Leu Tyr Ile	
81 145 150 155 160	
83 tca ccg cgc ctc acc ttc ccc tca ctc cag gcc ctg gtg gac cat tac	528
84 Ser Pro Arg Leu Thr Phe Pro Ser Leu Gln Ala Leu Val Asp His Tyr	
85 165 170 175	
87 tct gag ctg gc ^g gat gac atc tgc tgc cta ctc aag gag ccc tgt gtc	576
88 Ser Glu Leu Ala Asp Asp Ile Cys Cys Leu Leu Lys Glu Pro Cys Val	
89 180 185 190	
91 ctg cag agg gct ggc ccg ctc cct ggc aag gat ata ccc cta cct gtg	624
92 Leu Gln Arg Ala Gly Pro Leu Pro Gly Lys Asp Ile Pro Leu Pro Val	
93 195 200 205	
95 act gtg cag agg aca cca ctc aac tgg aaa gag ctg gac agc tcc ctc	672
96 Thr Val Gln Arg Thr Pro Leu Asn Trp Lys Glu Leu Asp Ser Ser Leu	
97 210 215 220	
99 ctg ttt tct gaa gct gcc aca ggg gag gag tct ctt ctc agt gag ggt	720
100 Leu Phe Ser Glu Ala Ala Thr Gly Glu Glu Ser Leu Leu Ser Glu Gly	
101 225 230 235 240	
103 ctc ccg gag tcc ctc agc ttc tac atc agc ctg aat gac gag gct gtc	768
104 Leu Arg Glu Ser Leu Ser Phe Tyr Ile Ser Leu Asn Asp Glu Ala Val	
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108 Ser Leu Asp Asp Ala	
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113 <211> LENGTH: 261	
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115 <213> ORGANISM: Homo sapiens	
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127 Ser Lys Ala Thr Ala Val Ala Leu Gly Ser Phe Pro Ala Gly Gly Pro	

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131 Ala Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile Val Ser Glu
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135 Asp Gly Asp Trp Trp Thr Val Leu Ser Glu Val Ser Gly Arg Glu Tyr
136 65      70          75          80
139 Asn Ile Pro Ser Val His Val Ala Lys Val Ser His Gly Trp Leu Tyr
140      85          90          95
143 Glu Gly Leu Ser Arg Glu Lys Ala Glu Glu Leu Leu Leu Pro Gly
144      100         105         110
147 Asn Pro Gly Gly Ala Phe Leu Ile Arg Glu Ser Gln Thr Arg Arg Gly
148      115         120         125
151 Ser Tyr Ser Leu Ser Val Arg Leu Ser Arg Pro Ala Ser Trp Asp Arg
152      130         135         140
155 Ile Arg His Tyr Arg Ile His Cys Leu Asp Asn Gly Trp Leu Tyr Ile
156 145      150         155         160
159 Ser Pro Arg Leu Thr Phe Pro Ser Leu Gln Ala Leu Val Asp His Tyr
160      165         170         175
163 Ser Glu Leu Ala Asp Asp Ile Cys Cys Leu Leu Lys Glu Pro Cys Val
164      180         185         190
167 Leu Gln Arg Ala Gly Pro Leu Pro Gly Lys Asp Ile Pro Leu Pro Val
168      195         200         205
171 Thr Val Gln Arg Thr Pro Leu Asn Trp Lys Glu Leu Asp Ser Ser Leu
172      210         215         220
175 Leu Phe Ser Glu Ala Ala Thr Gly Glu Glu Ser Leu Leu Ser Glu Gly
176 225      230         235         240
179 Leu Arg Glu Ser Leu Ser Phe Tyr Ile Ser Leu Asn Asp Glu Ala Val
180      245         250         255
183 Ser Leu Asp Asp Ala
184      260
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 276
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199      20          25          30
202 Tyr Pro Ser Pro Asp Ile Ser Pro Pro Ile Phe Arg Arg Gly Glu Lys
203      35          40          45
206 Leu Arg Val Ile Ser Asp Glu Gly Gly Trp Trp Lys Ala Ile Ser Leu
207      50          55          60
210 Ser Thr Gly Arg Glu Ser Tyr Ile Pro Gly Ile Cys Val Ala Arg Val
211 65      70          75          80
214 Tyr His Gly Trp Leu Phe Glu Gly Leu Gly Arg Asp Lys Ala Glu Glu
215      85          90          95
218 Leu Leu Gln Leu Pro Asp Thr Lys Val Gly Ser Phe Met Ile Arg Glu
219      100         105         110
222 Ser Glu Thr Lys Lys Gly Phe Tyr Ser Leu Ser Val Arg His Arg Gln

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223	115	120	125
226	Val Lys His Tyr Arg Ile Phe Arg Leu Pro Asn Asn Trp Tyr Tyr Ile		
227	130	135	140
230	Ser Pro Arg Leu Thr Phe Gln Cys Leu Glu Asp Leu Val Asn His Tyr		
231	145	150	155
234	Ser Glu Val Ala Asp Gly Leu Cys Cys Val Leu Thr Thr Pro Cys Leu		160
235	165	170	175
238	Thr Gln Ser Thr Ala Ala Pro Ala Val Arg Ala Ser Ser Ser Pro Val		
239	180	185	190
242	Thr Leu Arg Gln Lys Thr Val Asp Trp Arg Arg Val Ser Arg Leu Gln		
243	195	200	205
246	Glu Asp Pro Glu Gly Thr Glu Asn Pro Leu Gly Val Asp Glu Ser Leu		
247	210	215	220
250	Phe Ser Tyr Gly Leu Arg Glu Ser Ile Ala Ser Tyr Leu Ser Leu Thr		
251	225	230	235
254	Ser Glu Asp Asn Thr Ser Phe Asp Arg Lys Lys Lys Ser Ile Ser Leu		240
255	245	250	255
258	Met Tyr Gly Gly Ser Lys Arg Lys Ser Ser Phe Phe Ser Ser Pro Pro		
259	260	265	270
262	Tyr Phe Glu Asp		
263	275		

VERIFICATION SUMMARY

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Output Set: N:\CRF4\12022002\J043649.raw

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